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Plasminogen Activator Inhibitor-1 and Diagnosis of the Metabolic Syndrome in a West African Population

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***Background*—**Metabolic syndrome (MetS) is diagnosed by the presence of at least 3 of the following: obesity, hypertension, hyperglycemia, hypertriglyceridemia, and low high-density lipoprotein. Individuals with MetS also typically have elevated plasma levels of the antifibrinolytic factor, plasminogen activator inhibitor-1 (PAI-1), but the relationships between PAI-1 and MetS diagnostic criteria are not clear. Understanding these relationships can elucidate the relevance of MetS to cardiovascular disease risk, because PAI-1 is associated with ischemic events and directly involved in thrombosis.

***Methods and Results*—**In a cross-sectional analysis of 2220 Ghanaian men and women from urban and rural locales, we found the age-standardized prevalence of MetS to be as high as 21.4% (urban women). PAI-1 level increased exponentially as the number of diagnostic criteria increased linearly ($P<10^{-13}$), supporting the conclusion that MetS components have a joint effect that is stronger than their additive contributions. Body mass index, triglycerides, and fasting glucose were more strongly correlated with PAI-1 than with canonical MetS criteria, and this pattern did not change when pair-wise correlations were conditioned on all other risk factors, supporting an independent role for PAI-1 in MetS. Finally, whereas the correlations between conventional risk factors did not vary significantly by sex or across urban and rural environments, correlations with PAI-1 were generally stronger among urban participants.

***Conclusions*—**MetS prevalence in the West African population we studied was comparable to that of the industrialized West. PAI-1 may serve as a key link between MetS, as currently defined, and the endpoints with which it is associated. Whether this association is generalizable will require follow-up. **(*J Am Heart Assoc*. 2016;5:e003867 doi: 10.1161/JAHA.116.003867)**

Key Words: diabetes mellitus • epidemiology • fibrinolysis • hypertension • lipids • obesity

Metabolic syndrome (MetS) is a set of cardiometabolic abnormalities that cluster in people at increased risk for coronary heart disease and type 2 diabetes mellitus. Any 3 of the cardiovascular risk factors of obesity, hypertension, hyperglycemia, hypertriglyceridemia, and low high-density lipoprotein (HDL) are sufficient for diagnosis of MetS, according to a recent consensus statement.[1] Although it is well known that these risk factors co-occur more often than expected by chance, the reasons for their co-occurrence are not clear. The implications are also unclear, with recent debate centered on whether multiple risk factors have a joint effect on cardiovascular risk greater than the sum of their individual contributions.[2–4] If the increased risk attributed to MetS can be wholly accounted for by the additive contributions of its component conditions, arguably little can be gained by studying the risk factors collectively.

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Accompanying Tables S1 through S4 and Figure S1 are available at http://jaha.ahajournals.org/content/5/10/e003867/DC1/embed/inline-supplementary-material-1.pdf

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There is, however, at least 1 aspect of the syndrome that may distinguish it from its component conditions: Patients diagnosed with MetS typically suffer from a hypercoagulable condition of the blood, caused by supranormal levels of clotting and antifibrinolytic factors.[5,6] Among the most prominent of these factors is plasminogen activator inhibitor 1 (PAI-1), which hinders clot degradation by inhibiting plasminogen activators in the fibrinolytic pathway.[7] PAI-1 appears to be connected to MetS in multiple ways beyond this antifibrinolytic role. For example, at high levels, PAI-1 promotes a chronic state of low-grade inflammation, one of the proposed underlying causes of MetS.[8,9] A number of proinflammatory factors are known to stimulate PAI-1 production, including interleukins, tumor necrosis factor alpha, transforming growth factor beta, and C-reactive protein.[7,10,11] Although circulating PAI-1 is mainly released by hepatic and endothelial cells, adipose tissue becomes a major source as visceral adiposity increases, which also has been implicated in increased inflammation and coronary heart disease.[12,13] High PAI-1 may also predispose patients to premature atherosclerosis not only through inflammatory pathways, but also by interfering with cell migration.[13,14] Other PAI-1 stimulants related to MetS include plasma glucose, insulin, very low-density lipoprotein (VLDL) cholesterol, and the vasopressive hormone, angiotensin II.[15,16]

Perhaps, most important, PAI-1 represents a natural link between MetS risk factors and acute phases of cardiovascular disease.[16,17] Circadian spikes in PAI-1 levels likely explain the morning peak in the incidence of myocardial infarction and stroke,[18] and epidemiological studies have demonstrated a positive association between elevated plasma PAI-1 levels and adverse cardiovascular events.[7,15,19] Thus, understanding how PAI-1 levels respond to the risk factors of MetS (and vice versa) should provide insight into how the components of the syndrome individually—and jointly—increase the risk of cardiovascular disease.

There have been relatively few studies of MetS in West Africa, and no large study, to our knowledge, has addressed the association between PAI-1 and MetS in the region. Prevalence and etiology of MetS, including its relationship with PAI-1, vary among ethnic groups,[20,21] making it important to study these factors simultaneously in different populations. In addition, urbanization and the changes that accompany it, such as the adoption of sedentary lifestyle and nutrient-poor, calorie-rich diets, are major factors in MetS prevalence and etiology,[22,23] but no study, to our knowledge, has examined how urban-rural differences may affect the relationship between PAI-1 and MetS.

Here, we present a multivariate analysis of MetS and PAI-1, using cardiovascular risk factor data from 3331 men and women in Ghana from both urban and rural locales. We assess the correlational architecture of MetS risk factors and estimate their potential relevance to thrombotic endpoints by using strength and independence of association with PAI-1 as a proxy. Because correlational analyses do not require any assumptions of direction of effect, they are well suited for the study of metabolic systems.[24] Partial correlations in particular can distinguish independent (and possibly direct) interactions among risk factors from merely incidental associations. In addition, we assess the possibility of nonlinear relationships among risk factors, such as at the extremes of their distributions, which may be especially pertinent to clinical outcomes. Throughout, we evaluate how the patterns of association we observe may be influenced by differences in sex and environment (urban vs rural), both of which have been shown to affect cardiovascular disease risk.[25,26] The overriding goal of this study was to assess the extent to which PAI-1 may play a central or connecting role in the diagnosis of MetS.

Methods

Study Population

Participants were recruited from Sunyani, the capital of the Brong Ahafo region of Ghana (population 250 000 as of the 2012 census), and from surrounding rural villages of fewer than 5000 people. Urban recruitment occurred from 2002 to 2007. Rural participants were recruited in 2008. Participants learned about the study at public venues, including local churches and markets. Individuals <18 years of age or who were first- or second-degree relatives of someone already enrolled in the study were excluded. Participants provided information by in-person interviews regarding their medical histories and other demographic and socioeconomic factors, including education level, smoking status, alcohol consumption, and current medications. All participants provided informed consent. Institutional review boards at Dartmouth College (Hanover, NH), Vanderbilt University (Nashville, TN), and Regional Hospital, Sunyani approved all protocols.

Anthropometric Measurements and Biochemical Analyses

The mean of 2 measurements for both systolic blood pressure (SBP) and diastolic blood pressure (DBP) was calculated. Blood was drawn between 8:00 and 10:00 AM, after a fast ≥8 hours, and used to assess fasting glucose, fasting lipids, and PAI-1 levels. Glucose was measured from blood drops using a SureStep monitor by LifeScan (Milpitas, CA). Total cholesterol (TC), triglycerides (TG), and HDL levels were measured in plasma. PAI-1 antigen was measured using an enzyme-linked immunoassay (Biopool AB, Umea, The

Netherlands). Here, only total PAI-1 was measured (comprising free PAI-1 as well as its complexes with plasminogen activators), given that the short half-life of the active molecule in plasma makes it less useful for studies of chronic disease. Body mass index (BMI) was calculated with weight and height measurements (kg/m^2).

Study Variables

Five categorical metabolic risk factors (hypertriglyceridemia, low HDL, hypertension, hyperglycemia, and obesity) were defined according to the updated National Cholesterol Education Program Adult Treatment Panel-III (NCEP ATP-III) criteria,[27] as follows: TG ≥150 mg/dL; HDL <40 mg/dL in males or <50 mg/dL in females; SBP and DBP ≥130/85 mm Hg or on antihypertensive medication; fasting glucose (GLUC) ≥100 mg/dL or on antidiabetic medication; and BMI ≥30. None of the study participants reported taking statins. Mean arterial pressure (MAP) was calculated using the formula: MAP=DBP+[(SBP−DBP)/3], which approximates the average arterial pressure during a single cardiac cycle. Because MAP has been shown to predict future MetS more accurately than SBP, DBP, or pulse pressure,[28] it was used in the correlational analyses. Pearson's correlation coefficients and tests of correlational homogeneity are sensitive to deviations from normality.[29,30] Quantitative variables used in the correlational analyses were therefore log-transformed after observing that this improved approximations to normality (using the Shapiro-Wilk test as a criterion). For clarity of presentation, however, mention in the text does not reflect these transformations (eg, as "ln-glucose" or "ln-PAI-1," etc).

For calculating prevalence of MetS, the study participants for whom no data were missing (N=2220) and who had at least 3 of the 5 conditions (as per the NCEP ATP-III guidelines[1]) were deemed cases. The missing data for 1111 participants (598 urban, 513 rural) resulted from a supply failure for HDL cholesterol assay during the collection process.

Statistical Analyses

Prevalence rates of MetS were age-standardized to the World Health Organization 2000–2025 standard population using recommended age bins that pertained to our data (18–24, 25–34, 35–44, 45–54, and ≥55 years-old).[31,32] Relative risks (RRs) of MetS (for urban vs rural and female vs male) were also estimated. To check for possible bias in the participants with missing HDL data versus complete cases, the age-adjusted means and variances of all other variables were compared (by *t* test and Levene's test, respectively) for both groups.

Pair-wise correlations between BMI, MAP, GLUC, TG, HDL, and PAI-1 were calculated, using the residuals after linear regression on age, sex, and residence. Pair-wise correlations were also calculated separately for (1) individuals stratified by residence (after age and sex adjustment) and (2) individuals stratified by sex (after age and residence adjustment). Tests for homogeneity of correlation between groups (ie, urban vs rural, male vs female) were conducted by *t* test after Fisher transformation of correlation coefficients.[33] For every pair of variables in the set of BMI, MAP, GLUC, TG, HDL, and PAI-1, partial correlations were calculated controlling for the remaining variables in the set, after which the above analyses were repeated. For clarity, only these higher-order partial correlations are referred to as "partial correlations" in the text, although all correlations in this study are controlled for age and sex and/or residence.

The following approach was used to assess visually whether the strengths of association between MetS traits (BMI, MAP, GLUC, TG, and HDL) and PAI-1 were consistent over the entirety of their respective ranges, and to identify patterns of nonlinear association: (1) Age-, sex-, and residence-adjusted regression residuals of the five MetS traits were standardized, ranked in ascending order, and paired with corresponding standardized PAI-1 values; (2) the 25th percentile, median, and 75th percentile of PAI-1 (period=100) were plotted against the corresponding median (period=100) of each MetS trait; (3) smooth curves of the plots were generated, using a cubic spline method. Briefly, for n observations, where $\tilde{x}_i$ is the ith standardized median (period 100) of a risk factor, $i \in [1, n-99]$, and $\tilde{P}_i$ the corresponding quantile value of PAI-1, such that $\tilde{P}_i = \mu(\tilde{x}_i)$, the smoothing function $\hat{\mu}$ estimated μ by minimizing

$$\sum_{i=1}^{n-99} \left(\tilde{P}_i - \hat{\mu}(\tilde{x}_i)\right)^2 + \lambda \int_{x_1}^{x_2} \hat{\mu}''(\tilde{x})^2 d\tilde{x}$$

The first term represents the sum of squares error and the second term the penalty for "roughness." The parameter λ controls the bias-variance trade-off and was set to 10.[34] PAI-1 quartiles were used in these analyses rather than mean values to minimize the influence of outliers caused by the characteristic kurtosis of the PAI-1 distribution, and to gain insight into whether PAI-1 levels at upper or lower quartiles associate differently with changes in the other risk factors.

For further analysis, an ordinal variable, defined as the number of conditions with which an individual was diagnosed (ie, 0 through 5), was created to augment the dichotomous characterization of MetS (ie, as the presence or absence of at least 3 conditions). Mean PAI-1 was calculated for each of these groups, using the standardized age-, sex-, and residence-adjusted residuals. The association between

MetS progression and PAI-1 was then assessed in 2 ways. First, the number of MetS conditions was modeled as a function of PAI-1, using ordinal regression (with cumulative logit link), adding age, sex, and residence as covariates. PAI-1^2 was then added as an explanatory variable, and the fit of the quadratic versus the linear model was compared using the likelihood ratio test. Second, mean PAI-1 levels were compared by *t* test for each sequential pair of groups (ie, 0 vs 1 conditions, 1 vs 2, etc). A curve was also fitted to the PAI-1 means using polynomial regression (quadratic). Statistical analyses were performed using JMP Pro (12.1; SAS Institute Inc., Cary, NC), STATA (12; StataCorp LP, College Stattion, TX), and R software (3.2; R Foundation for Statistical Computing, Vienna, Austria).

Results

Of the 3331 participants in this study, 2276 (68%) were urban residents, of whom 1298 (57%) were female and 978 male. Of the 1055 rural residents, 583 (55%) were female and 472 male. Ages ranged from 18 to 99 and were similarly distributed among urban and rural men and women (*P*=0.23, Kruskal–Wallis test). In analyses that depended on the total number of categorical risk factors, participants with missing data were excluded, lowering the sample size to 2220. The decrease in sample size resulted from the lack of supplies for testing HDL cholesterol during the collection process. However, the distributions of measured variables between participants with and without missing data were not significantly different (Table S1), consistent with the sporadic and random timing of the supply shortages. Age-standardized MetS prevalence by group and summary data of associated variables are presented in Table 1 and Figure S1.

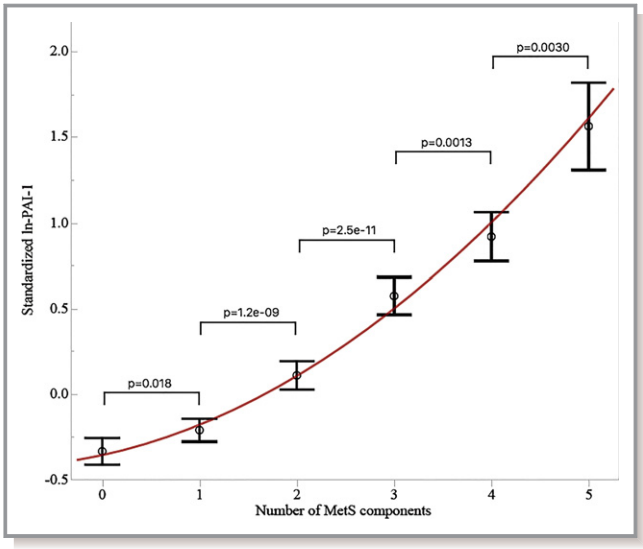

Figure 1. Relationship between the total number of risk factor diagnoses and mean PAI-1 concentrations. Horizontal axis: 2220 participants from the Brong Ahafo region of Ghana were grouped by number of risk factor conditions (obesity, hypertension, hyperglycemia, hypertriglyceridemia, and low HDL); 22 participants had all 5; 573 had 4; 473 had 3; 376 had 2; 300 had 1; and 573 had none. Vertical axis: For each group, mean standardized ln-PAI-1 concentrations (adjusted for age, sex, and urban/rural residence) are depicted with 95% CIs. *P* values above horizontal brackets are for *t* tests comparing the means of adjacent groups. PAI-1 was normally distributed within each group (Shapiro-Wilk test; *P*>0.05). The quadratic fit to the means is also depicted (R^2=0.996). HDL indicates high-density lipoprotein cholesterol; MetS, metabolic syndrome; PAI-1, plasminogen activator inhibitor 1.

Prevalence and RR of MetS

Male and female urban residents had a significantly higher RR of MetS than their rural counterparts (1.61 with 95% CI, 1.02–2.53, and 1.72 with 95% CI, 1.28–2.3, males and females,

Table 1. Prevalence of MetS and Its Component Risk Factors Among 2220 Urban and Rural Men and Women From Brong Ahafo, Ghana

	Males		Females	
	Urban	Rural	Urban	Rural
	N=721	N=225	N=957	N=317
MetS*	0.126 (0.102, 0.151)	0.078 (0.043, 0.113)	0.214 (0.188, 0.240)	0.112 (0.077, 0.147)
Obesity	0.065 (0.049, 0.086)	0.00 (0.00, 0.017)	0.265 (0.238, 0.294)	0.050 (0.031, 0.080)
Hypertension	0.130 (0.108, 0.157)	0.111 (0.076, 0.159)	0.097 (0.080, 0.118)	0.088 (0.062, 0.125)
Hyperglycemia	0.413 (0.378, 0.450)	0.267 (0.213, 0.328)	0.389 (0.358, 0.420)	0.293 (0.246, 0.346)
High TG	0.239 (0.209, 0.271)	0.173 (0.129, 0.228)	0.315 (0.286, 0.345)	0.293 (0.246, 0.346)
Low HDL-C	0.437 (0.401, 0.473)	0.391 (0.330, 0.456)	0.588 (0.557, 0.619)	0.612 (0.557, 0.664)

HDL-C indicates high-density lipoprotein cholesterol; MetS, metabolic syndrome; TG, triglycerides.
*Prevalence was age-standardized to the World Health Organization 2000–2025 standard population; N=sample size of participants for whom no data were missing; in parentheses: 95% CIs.

Table 2. Pearson Correlation Coefficients Between Cardiovascular Risk Factors Associated With MetS in Urban and Rural Ghanaians

						Rural				Urban				Homogeneity of Correlation
Trait 1	Trait 2	r^*	CI	N	*P* Value	$r^\dagger$	CI	N	*P* Value	$r^\dagger$	CI	N	*P* Value	*P* Value
BMI	PAI-1	0.43	(0.40, 0.45)	3331	<0.0001	0.29	(0.23, 0.34)	542	<0.0001	0.47	(0.44, 0.51)	2276	<0.0001	4.90E-09
BMI	GLUC	0.15	(0.12, 0.18)	3331	<0.0001	0.20	(0.14, 0.25)	1055	<0.0001	0.13	(0.09, 0.17)	2276	<0.0001	0.0621
BMI	HDL	−0.15	(−0.19, −0.11)	2225	<0.0001	−0.08	(−0.17, 0.00)	543	0.0522	−0.18	(−0.23, −0.13)	1682	<0.0001	0.0472
BMI	MAP	0.30	(0.27, 0.33)	3331	<0.0001	0.28	(0.22, 0.33)	1055	<0.0001	0.31	(0.27, 0.34)	2276	<0.0001	0.4186
BMI	TG	0.25	(0.22, 0.28)	3321	<0.0001	0.18	(0.13, 0.24)	1051	<0.0001	0.27	(0.23, 0.31)	2270	<0.0001	0.0122
GLUC	PAI-1	0.20	(0.16, 0.23)	3331	<0.0001	0.11	(0.05, 0.17)	1055	0.0004	0.23	(0.19, 0.27)	2276	<0.0001	9.90E-04
GLUC	HDL	−0.12	(−0.16, −0.08)	2225	<0.0001	−0.14	(−0.22, −0.05)	543	0.0014	−0.12	(−0.16, −0.07)	1682	<0.0001	0.6887
GLUC	MAP	0.13	(0.10, 0.17)	3331	<0.0001	0.17	(0.11, 0.23)	1055	<0.0001	0.11	(0.07, 0.16)	2276	<0.0001	0.1416
GLUC	TG	0.17	(0.14, 0.21)	3321	<0.0001	0.20	(0.14, 0.26)	1051	<0.0001	0.16	(0.12, 0.20)	2270	<0.0001	0.2878
HDL	PAI-1	−0.17	(−0.21, −0.13)	2225	<0.0001	−0.17	(−0.25, −0.08)	543	0.0001	−0.18	(−0.22, −0.13)	1682	<0.0001	0.8302
HDL	MAP	0.03	(−0.01, 0.07)	2225	0.1376	0.05	(−0.03, 0.14)	543	0.2110	0.03	(−0.02, 0.07)	1682	0.2752	0.5818
HDL	TG	−0.27	(−0.31, −0.23)	2220	<0.0001	−0.30	(−0.37, −0.22)	542	<0.0001	−0.26	(−0.31, −0.22)	1678	<0.0001	0.4726
MAP	PAI-1	0.23	(0.20, 0.26)	3331	<0.0001	0.24	(0.18, 0.29)	1055	<0.0001	0.23	(0.19, 0.27)	2276	<0.0001	0.7878
MAP	TG	0.16	(0.13, 0.20)	3321	<0.0001	0.19	(0.13, 0.25)	1051	<0.0001	0.15	(0.11, 0.19)	2270	<0.0001	0.2561
TG	PAI-1	0.35	(0.32, 0.38)	3321	<0.0001	0.28	(0.22, 0.33)	1051	<0.0001	0.38	(0.35, 0.42)	2270	<0.0001	2.10E-03

BMI indicates body mass index; GLUC, glucose; HDL, high-density lipoprotein cholesterol; MAP, mean arterial pressure; MetS, metabolic syndrome; PAI-1, plasminogen activator inhibitor 1; TG, triglycerides.

*Pearson correlation coefficient, calculated using residuals after adjustment for age, sex, and residence.

†Pearson correlation coefficient, calculated for urban and rural participants separately, using residuals after adjustment for age and sex; CI=95% confidence interval (in parenthesis); *P* value=probability of *r* if true correlation is zero; Homogeneity of Correlation *P* value=probability of these data if true correlation is equal for urban and rural populations.

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respectively). Urban women, who had the highest prevalence of obesity among all groups (26.5%), also had the highest age-standardized prevalence of MetS (21.4%; Table 1), with an RR of 1.68 (CI, 1.36–2.07) compared to urban men ($P<0.0001$), and 1.72 compared to rural women ($P=0.0002$). Among rural participants, risk of MetS did not differ by sex.

Relationship Between PAI-1 and Number of MetS Conditions

Mean PAI-1 (log-normalized and adjusted for age, sex, and residence) rose exponentially as the number of MetS risk factors increased linearly. The quadratic fit to the means was virtually perfect ($R^2=0.996$). Among participants who had at least 1 MetS risk factor, mean PAI-1 increased significantly with each additional condition, with the most significant increase occurring when the number of conditions increased from 2 to 3, consistent with the NCEP ATP-III definition (Figure 1). Ordinal polynomial regression was also used to model the number of MetS risk factors as a function of PAI-1. The improvement of the quadratic fit over the linear fit was highly significant ($P<10^{-13}$), confirming the strong exponential relationship between the logarithm of PAI-1 level and number of MetS criteria.

Pair-wise Correlations of Risk Factors

All pair-wise correlations between risk factors adjusted for age, sex, and residence were statistically significant ($P<0.0001$), except for the correlation between MAP and HDL (Table 2 and Figure 2). Seven of 15 correlations were at least 0.20 in magnitude: BMI-PAI-1; BMI-TG; BMI-MAP; TG-PAI-1; TG-HDL; MAP-PAI-1; and GLUC-PAI-1. The above analysis was repeated after stratifying participants by urban versus rural residence and adjusting for age and sex. Of the 5 pair-wise correlations with PAI-1, 3 were significantly stronger in the urban population: BMI ($P=4.9\times10^{-9}$); GLUC ($P=9.9\times10^{-4}$); and TG ($P=2.1\times10^{-3}$; Table 2 and Figure 2). Among pair-wise correlations that did not include PAI-1, only 2 of 10 pairs were significantly different: BMI-HDL ($P=0.047$) and BMI-TG ($P=0.012$), with both correlations again stronger in the urban population (Table 2 and Figure 2). When participants were stratified by sex, no P value for homogeneity of correlation was smaller than 0.01 (Table 3 and Figure 2). Of the 3 significant at the 0.05 level, the GLUC-PAI-1 correlation was higher in women than in men, and the correlations of both BMI and PAI-1 with MAP were higher in men.

Pair-wise Partial Correlations of Risk Factors

Partial correlations between pairs of risk factors (including PAI-1) that controlled for all other risk factors (in addition to age and sex and/or residence, as above) were calculated to assess strengths of independent association. All partial correlations were statistically significant, with 4 greater than 0.20 in magnitude: BMI-PAI-1; TG- PAI-1; BMI-MAP; and TG-HDL (Table 4 and Figure 3). Three of 15 partial correlations were significantly different between urban and rural residents (BMI-PAI-1, $P=0.0002$; GLUC-PAI-1, $P=0.001$; and BMI-GLUC, $P=0.005$), with the stronger correlations in the urban group (Table 4 and Figure 3). Only 1 of 15 partial correlations was significantly different between men and women (GLUC-PAI-1, $P=0.023$; Table 5 and Figure 3). The partial correlational analyses were repeated for MetS risk factors without PAI-1 and yielded comparable results (Tables S2 through S4).

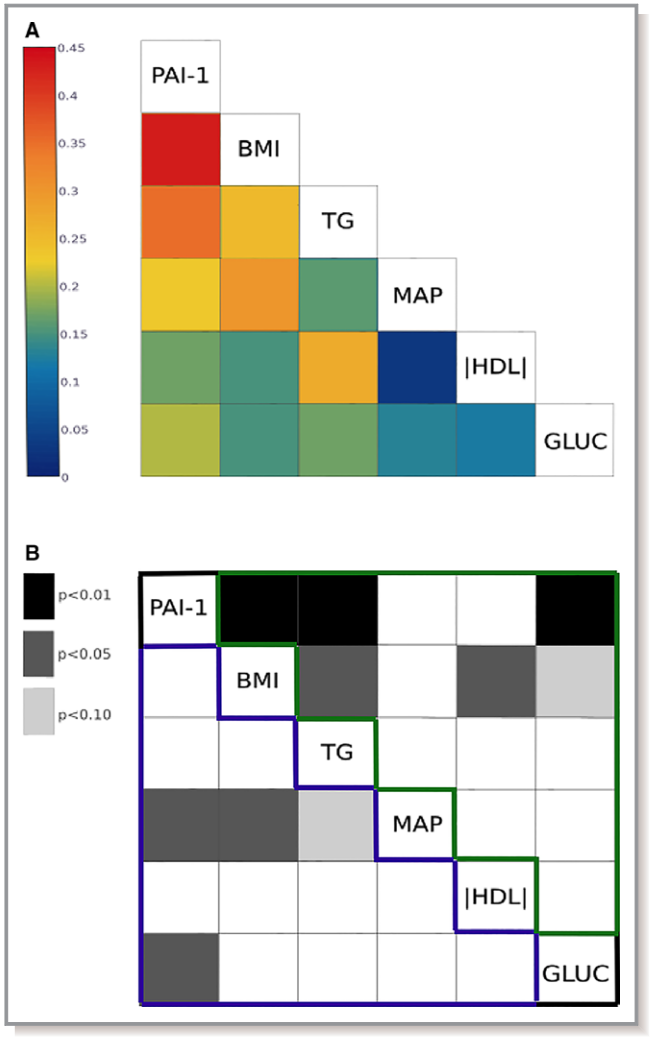

Figure 2. Strengths of correlation between cardiovascular risk factors associated with metabolic syndrome and their differences by sex and urban/rural residence. A, Colors in the heat map reflect the magnitude of correlation between risk factors adjusted for age, sex, and residence. In (B), shading reflects the statistical significance of differences in correlation by sex (below diagonal, purple) and residence (above diagonal, green). BMI indicates body mass index; GLUC, glucose; HDL, high-density lipoprotein cholesterol; MAP, mean arterial pressure; PAI-1, plasminogen activator inhibitor 1; TG, triglycerides.

Table 3. Pearson Correlation Coefficients Between Cardiovascular Risk Factors Associated With MetS, Including PAI-1, by Sex

		Females				Males				Homogeneity of Correlation *P* Value
Trait 1	Trait 2	*r*	CI	N	*P* Value	*r*	CI	N	*P* Value	
BMI	PAI-1	0.44	(0.41, 0.48)	1881	<0.0001	0.41	(0.36, 0.45)	1450	<0.0001	0.2008
BMI	GLUC	0.15	(0.10, 0.19)	1881	<0.0001	0.17	(0.12, 0.22)	1450	<0.0001	0.5756
BMI	HDL	−0.15	(−0.20, −0.10)	1275	<0.0001	−0.17	(−0.23, −0.11)	950	<0.0001	0.6037
BMI	MAP	0.27	(0.23, 0.32)	1881	<0.0001	0.35	(0.30, 0.39)	1450	<0.0001	0.0186
BMI	TG	0.24	(0.19, 0.28)	1878	<0.0001	0.27	(0.23, 0.32)	1443	<0.0001	0.2610
GLUC	PAI-1	0.23	(0.19, 0.28)	1881	<0.0001	0.15	(0.10, 0.20)	1450	<0.0001	0.0116
GLUC	HDL	−0.13	(−0.18, −0.07)	1275	<0.0001	−0.12	(−0.18, −0.05)	950	0.0003	0.7984
GLUC	MAP	0.11	(0.07, 0.16)	1881	<0.0001	0.16	(0.11, 0.21)	1450	<0.0001	0.1371
GLUC	TG	0.19	(0.14, 0.23)	1878	<0.0001	0.15	(0.10, 0.20)	1443	<0.0001	0.3103
HDL	PAI-1	−0.20	(−0.25, −0.15)	1275	<0.0001	−0.14	(−0.20, −0.08)	950	<0.0001	0.1569
HDL	MAP	0.05	(0.00, 0.11)	1275	0.0604	0.01	(−0.06, 0.07)	950	0.8036	0.2993
HDL	TG	−0.26	(−0.31, −0.20)	1274	<0.0001	−0.28	(−0.34, −0.23)	946	<0.0001	0.4758
MAP	PAI-1	0.20	(0.15, 0.24)	1881	<0.0001	0.27	(0.22, 0.32)	1450	<0.0001	0.0239
MAP	TG	0.13	(0.09, 0.18)	1878	<0.0001	0.19	(0.14, 0.24)	1443	<0.0001	0.0830
TG	PAI-1	0.34	(0.30, 0.38)	1878	<0.0001	0.36	(0.31, 0.40)	1443	<0.0001	0.5472

r=Pearson correlation coefficient, calculated using residuals after adjustment for age and residence by sex; CI=95% confidence interval (in parenthesis); *P* value=probability of *r* if true correlation is zero; Homogeneity of Correlation *P* value=probability of these data if true correlation is equal for men and women. BMI indicates body mass index; GLUC, glucose; HDL, high-density lipoprotein cholesterol; MAP, mean arterial pressure; MetS, Metabolic Syndrome; PAI-1, plasminogen activator inhibitor 1; TG, triglycerides.

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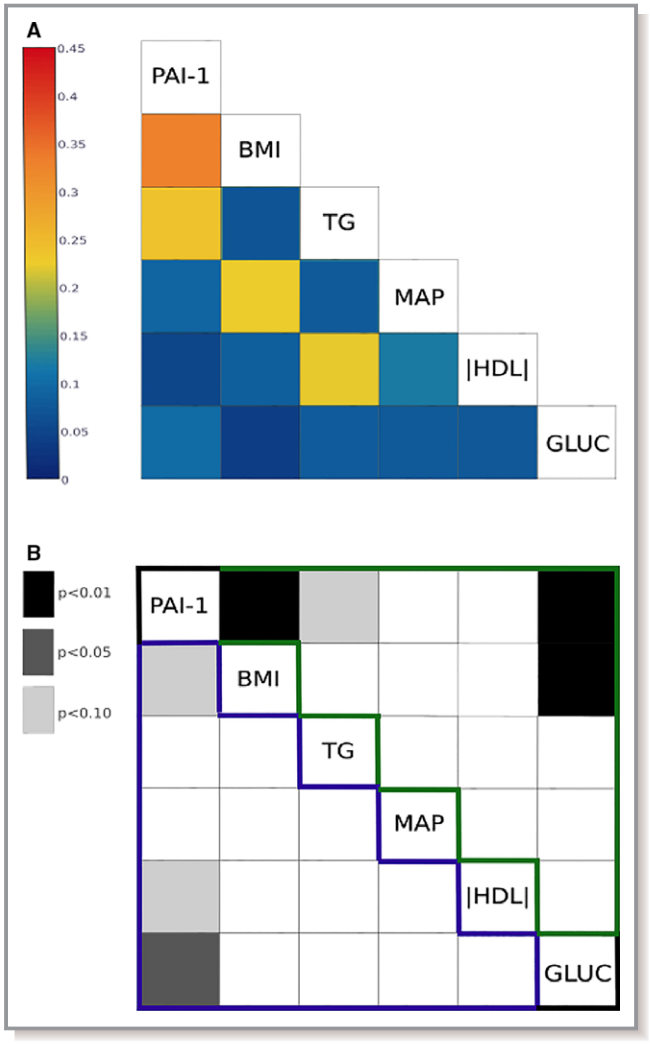

Figure 3. Strengths of partial correlation between cardiovascular risk factors associated with metabolic syndrome, including PAI-1, and their differences by sex and urban/rural residence. A, Colors in the heat map reflect the magnitude of partial correlation between risk factor pairs adjusted for all remaining risk factors, as well as age, sex, and residence. In (B), shading reflects the statistical significance of differences in partial correlation by sex (below diagonal, purple) and residence (above diagonal, green). BMI indicates body mass index; GLUC, glucose; HDL, high-density lipoprotein cholesterol; MAP, mean arterial pressure; PAI-1, plasminogen activator inhibitor 1; TG, triglycerides.

Relationship Between PAI-1 Quartiles and MetS Risk Factors

Consistent with the strong correlations, median PAI-1 increased most with BMI and TG, from ≈0.5 SD below the mean to 1.0 SD above (Figure 4). Notably, median PAI-1 did not vary when BMI was less than ≈1 SD below its mean. The relationship between PAI-1 quartiles and glucose displayed an abrupt shift at a glucose value of ≈+1.5 SD, from strongly positive to flat (Figure 4). The moving quartiles of PAI-1 were also evaluated for data stratified by sex and residence (Figure 5), revealing pronounced differences in the urban/rural PAI-1 quartiles. In contrast, the male-female trajectories of PAI-1 were almost indistinguishable, regardless of risk factor. The significantly different correlations by sex observed for PAI-1-MAP and PAI-1-GLUC, however, were likely reflected in the slight discordances at the right tails of their distributions (Figure 5).

To complement the partial correlational analyses, which assessed the independence of association among risk factors, PAI-1 quartiles were also plotted against each risk factor after adjustment for all others (Figure 4). The relationship of PAI-1 quartiles with all variables except BMI changed qualitatively with these additional adjustments. The most consistent difference was that independent associations with PAI-1 were much weaker when risk factors were below their means (Figure 4). Over their entire ranges, MAP and HDL had the weakest independent associations with PAI-1, corresponding to weak partial correlations ($r<0.10$). In contrast, the independent association between glucose and median PAI-1 was relatively strong, despite a similarly weak GLUC-PAI-1 partial correlation ($r<0.10$; Figure 4).

Discussion

A much-discussed topic has been whether the clustering of factors associated with MetS increases total cardiovascular disease risk in an additive or exponential way.[35–38] If, as observed here, PAI-1 increases exponentially as MetS diagnostic conditions increase linearly, then the question of whether MetS is "more than the sum of its parts" can be reduced, in part, to the clinical consequences of elevated PAI-1. Although the added value of using elevated PAI-1 as a prognostic indicator of adverse cardiac events has been debated,[39] its connection with increased cardiovascular risk has been demonstrated convincingly by many clinical and epidemiological studies.[7,40–44] Our results therefore support the basis of MetS as a clinical entity with distinct outcomes. We also observed the most significant increase in PAI-1 when the number of risk factors increased from 2 to 3, which supports the current NCEP ATP-III definition.

We found that the correlations between PAI-1 and the factors that define MetS (BMI, MAP, HDL, TG, and GLUC) were generally stronger than the correlations between the factors themselves. Given that MetS is essentially defined by the association of multiple risk factors, our results raise the question of whether PAI-1 should also be incorporated into its definition and diagnosis. For example, the strongest pair-wise correlations that included BMI, TG, or glucose were all with PAI-1. Moreover, this pattern did not change when we controlled for the influence of other factors, suggesting an independent role for PAI-1 in the clinical pathology of MetS.

Table 4. Pearson Partial Correlation Coefficients Between Pairs of Cardiovascular Risk Factors Associated With MetS, Including PAI-1, in 2220 Urban and Rural Ghanaians

					Rural				Urban				Homogeneity of Correlation *P* Value
Trait 1	Trait 2	*r**	CI	*P* Value	*r*†	CI	N	*P* Value	*r*†	CI	N	*P* Value	
BMI	PAI-1	0.33	(0.29, 0.37)	<0.0001	0.21	(0.12, 0.29)	542	<0.0001	0.37	(0.33, 0.41)	1678	<0.0001	0.0002
BMI	GLUC	0.04	(0.00, 0.08)	0.0564	0.13	(0.05, 0.21)	542	0.0023	−0.01	(−0.05, 0.04)	1678	0.7965	0.0054
BMI	HDL	−0.09	(−0.13, −0.04)	<0.0001	−0.03	(−0.12, 0.05)	542	0.4282	−0.12	(−0.16, −0.07)	1678	<0.0001	0.1003
BMI	MAP	0.22	(0.18, 0.26)	<0.0001	0.20	(0.12, 0.28)	542	<0.0001	0.23	(0.19, 0.28)	1678	<0.0001	0.4607
BMI	TG	0.07	(0.03, 0.11)	0.0007	0.05	(−0.03, 0.14)	542	0.2241	0.07	(0.03, 0.12)	1678	0.0027	0.6733
GLUC	PAI-1	0.10	(0.06, 0.14)	<0.0001	−0.01	(−0.09, 0.07)	542	0.8199	0.15	(0.10, 0.20)	1678	<0.0001	0.0010
GLUC	HDL	−0.08	(−0.12, −0.04)	0.0003	−0.09	(−0.18, −0.01)	542	0.0299	−0.07	(−0.12, −0.02)	1678	0.0030	0.6723
GLUC	MAP	0.08	(0.04, 0.12)	0.0002	0.11	(0.02, 0.19)	542	0.0113	0.07	(0.02, 0.11)	1678	0.0058	0.3994
GLUC	TG	0.08	(0.04, 0.12)	0.0001	0.12	(0.04, 0.20)	542	0.0046	0.06	(0.01, 0.11)	1678	0.0126	0.2171
HDL	PAI-1	−0.05	(−0.09, −0.01)	0.0156	−0.11	(−0.20, −0.03)	542	0.0085	−0.03	(−0.08, 0.01)	1678	0.1626	0.1090
HDL	MAP	0.12	(0.08, 0.16)	<0.0001	0.14	(0.05, 0.22)	542	0.0014	0.12	(0.07, 0.17)	1678	<0.0001	0.7363
HDL	TG	−0.22	(−0.26, −0.18)	<0.0001	−0.26	(−0.33, −0.18)	542	<0.0001	−0.21	(−0.25, −0.16)	1678	<0.0001	0.3053
MAP	PAI-1	0.09	(0.05, 0.13)	<0.0001	0.15	(0.07, 0.23)	542	0.0004	0.07	(0.03, 0.12)	1678	0.0024	0.1068
MAP	TG	0.08	(0.04, 0.12)	<0.0001	0.13	(0.04, 0.21)	542	0.0034	0.06	(0.02, 0.11)	1678	0.0094	0.2049
TG	PAI-1	0.24	(0.20, 0.28)	<0.0001	0.18	(0.10, 0.26)	542	<0.0001	0.26	(0.22, 0.31)	1678	<0.0001	0.0810

BMI indicates body mass index; GLUC, glucose; HDL, high-density lipoprotein cholesterol; MAP, mean arterial pressure; MetS, metabolic syndrome; PAI-1, plasminogen activator inhibitor 1; TG, triglycerides.

*Pearson correlation coefficient, calculated using residuals after adjustment for age, sex, and residence.

†Pearson correlation coefficient, calculated for urban and rural participants separately, using residuals after adjustment for age and sex; CI=95% confidence interval (in parenthesis); *P* value=probability of *r* if true partial correlation is zero; Homogeneity of Correlation *P* value=probability of these data if true partial correlation is equal for urban and rural.

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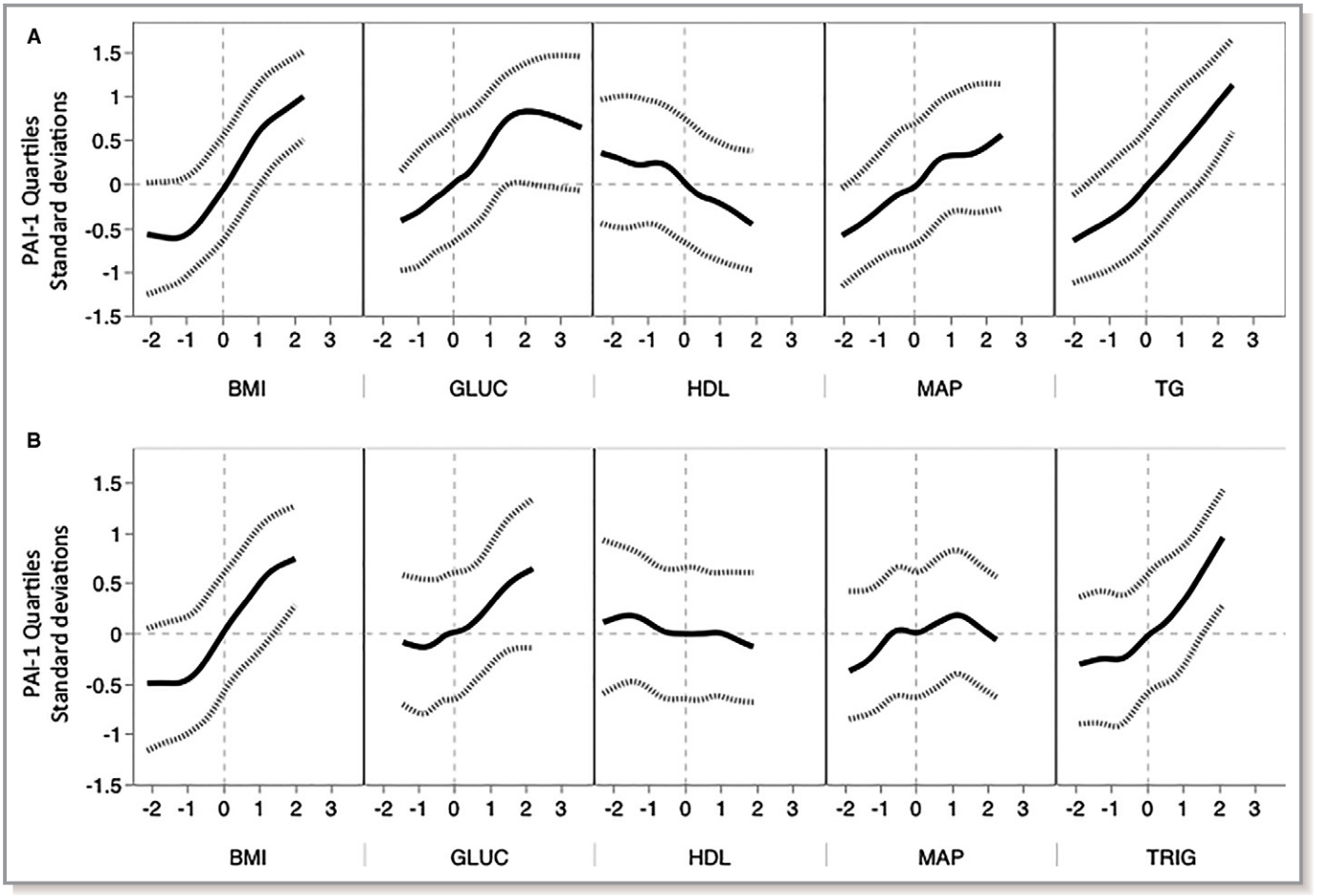

Figure 4. PAI-1 quartiles as a function of standardized MetS risk factor values. A, Medians (solid) and first and third quartiles (dotted) of standardized ln-PAI-1 after all data were adjusted for age, sex, and residence; in (B), data were further adjusted for the other risk factors. Period for quartiles=100. Data smoothed using cubic spline. BMI indicates body mass index; GLUC, glucose; HDL, high-density lipoprotein cholesterol; MAP, mean arterial pressure; MetS, metabolic syndrome; TRIG, triglycerides.

Because PAI-1 plays a direct biochemical role in thrombosis, each MetS factor's strength of correlation with PAI-1 may be indicative of its relevance to MetS-related cardiac events. Partial correlations with PAI-1 may be particularly relevant, because independent associations are more likely to reflect direct biochemical and physiological connections. In this regard, the strongest partial correlation we observed, that between PAI-1 and BMI, is consistent with the known biological mechanism of PAI-1 release from adipocytes. Adipokines also amplify PAI-1 expression through inflammatory pathways,[45] whereas PAI-1 itself may promote accumulation of visceral fat,[46] perhaps by mediating insulin signaling.[47–49] The second strongest partial correlation we observed was between PAI-1 and TG, likely influenced by the fact that the PAI-1 promoter is responsive to VLDL, which transports TG.[50] A similar connection exists between PAI-1 and the renin-angiotensin system, involved in hypertension.[51]

None of the partial correlations among the 5 MetS risk factors varied by sex or urban/rural environment when PAI-1 was excluded from analyses, despite differences in the underlying male/female and urban/rural risk factor distributions. This correlational homogeneity among conventional MetS criteria suggests that the relationships among risk factors are likely stable over a wide range of values and fairly insensitive to differences in physiological background, environment, and lifestyle. In contrast, the positive correlation of BMI, TG, and glucose with PAI-1 was markedly stronger in the urban population. To the extent that elevated PAI-1 increases the risk of thrombotic endpoints, then, it is possible that high BMI, TG, and glucose confer greater risk in urban than in rural environments. It is therefore likely that undefined aspects of the urban environment influence the nature of the relationships between adiposity, fasting glucose, TG, and PAI-1. In addition to obesity, factors such as stress and nutrient-poor diets have been shown to influence PAI-1 expression directly in animal models,[52,53] making these possible candidates as effect modifiers.

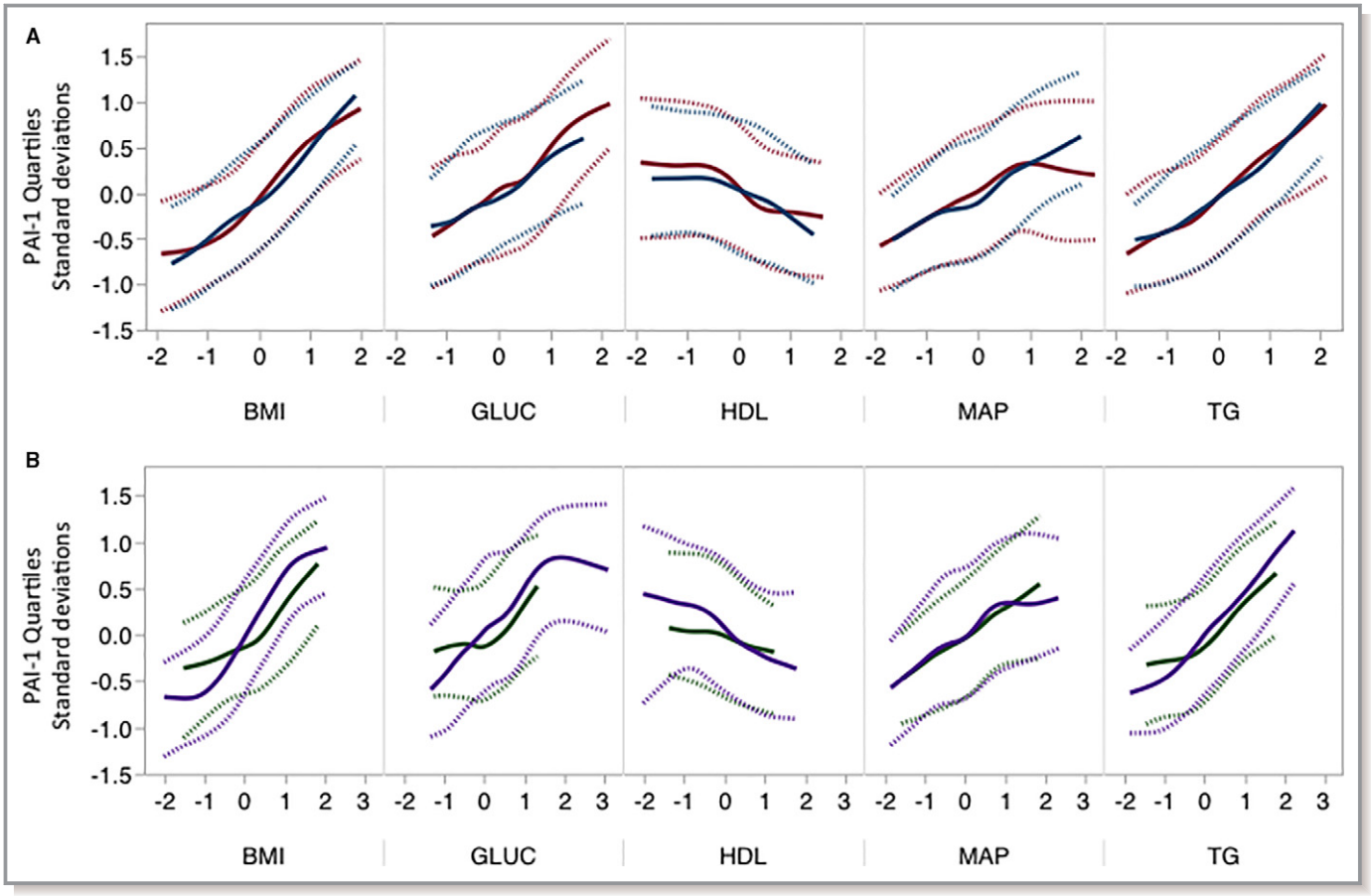

Figure 5. PAI-1 quartiles as a function of standardized MetS risk factor values, by sex and urban/rural residence. A, Medians (solid) and first and third quartiles (dotted) of standardized ln-PAI-1 values (period=100) for men (blue) and women (red); data adjusted for age and urban/rural residence, and smoothed using cubic spline. B, Medians (solid) and first and third quartiles (dotted) of standardized ln-PAI-1 values (period=100) for urban (purple) and rural (green) participants; data adjusted for age and sex, and smoothed using cubic spline. BMI indicates body mass index; GLUC, glucose; HDL, high-density lipoprotein cholesterol; MAP, mean arterial pressure; MetS, metabolic syndrome; TRIG, triglycerides.

Our results show that important physiological connections can be underestimated by a single correlation coefficient. For example, the correlation between glucose and PAI-1 was likely the result of 2 different patterns of association, which shifted at higher glucose values. Importantly, when glucose was less than ≈2 SDs above the mean, its relationship with PAI-1 quartiles was comparable to the stronger BMI-PAI-1 and TG-PAI-1 relationships. Similar analyses of PAI-1 quartiles using the residuals of the partial correlations confirmed this. The strong, independent connection over most of the normal glucose range may, in part, reflect increasing insulin resistance, which amplifies PAI-1 expression by accelerating the release of free fatty acids.[54]

Although we could not find similar studies with which to compare our higher-order partial correlations directly, a recent meta-analysis of 85 000 people (of whom 7.8% were African American and the remainder European) reported pair-wise correlations between MetS risk factors adjusted for age and sex.[55] Among all 15 pair-wise correlations we assessed, only BMI-GLUC and BMI-HDL here (adjusted for age, sex, and residence) fell outside of the 95% CIs reported by the meta-analysis. That study reported $r=-0.33$ for BMI-HDL and $r=0.28$ for BMI-GLUC, in contrast to our results of $r=-0.15$ and 0.15, respectively. With respect to HDL, this may be because many Ghanaians with normal BMI had low HDL. For example, 49% of participants with BMI below the obesity threshold had low HDL, and 25% of the participants with at least 1 risk factor had low HDL as the isolated condition. There may therefore be aspects of the Ghanaian environment, perhaps including diets, that contribute to low HDL in the absence of other risk factors. Speculation regarding the difference in the GLUC-PAI-1 correlation is more difficult, but we note that a previous study found a difference in the insulin-PAI-1 relationship between African and European women, which might provide some insight.[56]

MetS was significantly more prevalent in the urban population than the rural, and urban women were particularly at risk. Excess adiposity is generally considered the primary cause of MetS,[57] and the urban women had, by far,

Table 5. Pearson Partial Correlation Coefficients Between Cardiovascular Risk Factors Associated With MetS, Including PAI-1, by Sex

		Females				Males				
Trait 1	Trait 2	*r*	CI	N	*P* Value	*r*	CI	N	*P* Value	Homogeneity of Correlation *P* Value
BMI	PAI-1	0.35	(0.30, 0.40)	1274	<0.0001	0.29	(0.23, 0.34)	946	<0.0001	0.0814
BMI	GLUC	0.02	(−0.03, 0.08)	1274	0.4626	0.07	(0.00, 0.13)	946	0.0430	0.2920
BMI	HDL	−0.08	(−0.13, −0.02)	1274	0.0052	−0.11	(−0.17, −0.05)	946	0.0008	0.4682
BMI	MAP	0.21	(0.16, 0.26)	1274	<0.0001	0.26	(0.20, 0.32)	946	<0.0001	0.2487
BMI	TG	0.07	(0.01, 0.12)	1274	0.0142	0.09	(0.02, 0.15)	946	0.0067	0.6497
GLUC	PAI-1	0.14	(0.09, 0.20)	1274	<0.0001	0.05	(−0.02, 0.11)	946	0.1410	0.0233
GLUC	HDL	−0.07	(−0.12, −0.01)	1274	0.0128	−0.08	(−0.14, −0.01)	946	0.0202	0.8921
GLUC	MAP	0.06	(0.01, 0.12)	1274	0.0241	0.10	(0.04, 0.17)	946	0.0014	0.3414
GLUC	TG	0.10	(0.04, 0.15)	1274	0.0006	0.07	(0.00, 0.13)	946	0.0447	0.4765
HDL	PAI-1	−0.09	(−0.14, −0.03)	1274	0.0020	−0.01	(−0.08, 0.05)	946	0.6987	0.0842
HDL	MAP	0.13	(0.07, 0.18)	1274	<0.0001	0.12	(0.05, 0.18)	946	0.0004	0.7427
HDL	TG	−0.20	(−0.25, −0.14)	1274	<0.0001	−0.25	(−0.31, −0.19)	946	<0.0001	0.2210
MAP	PAI-1	0.07	(0.02, 0.13)	1274	0.0094	0.12	(0.06, 0.19)	946	0.0001	0.2363
MAP	TG	0.07	(0.01, 0.12)	1274	0.0134	0.09	(0.02, 0.15)	946	0.0078	0.6872
TG	PAI-1	0.22	(0.17, 0.27)	1274	<0.0001	0.25	(0.19, 0.31)	946	<0.0001	0.4270

r=Pearson partial correlation coefficient, calculated using residuals after adjustment for age and residence, by sex; CI=95% confidence interval; *P* value=probability of *r* if true partial correlation is zero; Homogeneity of Correlation *P* value=probability of these data if true partial correlation is equal for men and women. BMI indicates body mass index; GLUC, glucose; HDL, high-density lipoprotein cholesterol; MAP, mean arterial pressure; MetS, metabolic syndrome; PAI-1, plasminogen activator inhibitor 1; TG, triglycerides.

the highest prevalence of obesity. Nonetheless, the partial correlations between BMI and the other MetS risk factors in our study populations were surprisingly weak. Whereas cause cannot be inferred from correlation, it can be ruled out by the absence of correlation; therefore, the hypothesized causal connection between excess adiposity and MetS in African populations may not be straightforward. Simultaneous factors of susceptibility are probably involved. It is true that BMI serves as a somewhat crude variable for adiposity, in part because it does not necessarily reflect the distribution of body fat (eg, subcutaneous vs abdominal) on which the metabolic properties of adipocytes may depend.[58] Although waist circumference (WC) has often replaced BMI in studies of MetS, because increased abdominal fat is highly indicative of the MetS profile, it is not clear whether abdominal fat makes a greater contribution to total plasma PAI-1 than subcutaneous fat, particularly because stores of subcutaneous fat are typically much larger.[59–61] Moreover, some evidence indicates that WC may not be an effective measure of abdominal fat mass in African populations,[62] and that, even when measured accurately, abdominal fat may have a weaker relationship with plasma PAI-1 in Africans than in European-descent populations.[59,63]

The weak connection between obesity and MetS was particularly evident among rural males. Their age-standardized prevalence of MetS (7.8%) was unexpectedly high, despite no rural male participant's BMI being above the obesity threshold. Whereas "metabolically obese" individuals of normal weight are not uncommon in some populations (eg, South Asians),[64,65] often MetS without obesity reflects insulin resistance caused by factors other than excess adiposity.[66] However, 40% of the rural men who met the diagnostic criteria of MetS in our study did not have hyperglycemia in addition to hypertension and/or dyslipidemia (low HDL or high TG), making it unlikely that they were insulin resistant. MetS in the absence of obesity is also associated with the distribution of adipose tissue, which varies among populations[56,62,67,68] and may affect PAI-1 expression.[59] Thus, how comparable our rural participants are to others diagnosed with MetS is unclear, either from the standpoint of pathophysiology or clinical prognosis.

Some limitations of our study need to be acknowledged. The cross-sectional design of our study reduced our ability to elucidate causal relationships. Also, though our total sample size was relatively large, power was somewhat diminished after participants were stratified by sex and residence. Nonetheless, we identified highly significant findings in many of these stratified analyses. Our direct comparisons of higher- and lower-order partial correlations were further complicated by asymmetric power, owing to different numbers of adjustments. Additionally, though we performed these adjustments

to distinguish direct interactions among risk factors from merely incidental associations, we could only control for conventional risk factors, and, moreover, these risk factors have generally been defined on the bases of European studies.[69,70]

Our study explored the role of PAI-1 in MetS from multiple perspectives in an understudied population. Although urban residence and sex had dramatic effects on the mean values of cardiovascular risk factors, our partial correlational analyses revealed that the relationships among the factors used to diagnose MetS are remarkably stable. In contrast, the relationships between these factors and PAI-1 were more sensitive to such differences. Thus, urban-rural differences impacted not only MetS prevalence, but also patterns of clustering and association with PAI-1. Identifying the specific factors responsible for these phenomena should provide unique insight into MetS etiology and, where modifiable, could inform public health measures. The patterns we have identified, such as the exponential relationship between mean PAI-1 and MetS diagnostic conditions, and the nonlinear relationships between PAI-1 and some of the MetS risk factors, improve our understanding of how MetS may mediate cardiovascular disease risk, although generalizability to other populations will require further study. In summation, we provide evidence that the prothrombotic state may be more than a mere epiphenomenon of MetS, possibly playing a major role in its etiology and its clinical sequelae.

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Disclosures

None.

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Supplemental Material

Table S1. Comparison of risk factor distributions between participants with missing HDL measurements (N=1111) and those with full data (N=2220), by sex and residence.

Group	N, complete/ missing	Trait	standardized mean difference	95% CIL	95% CIU	p-value (t-test)	p-value (Levene's test)
URBAN MALES	721/257	PAI-1	-0.026	-0.169	0.117	0.721	0.132
		BMI	0.064	-0.079	0.206	0.381	0.956
		MAP	0.092	-0.031	0.216	0.143	0.299
		TRIG	-0.106	-0.230	0.018	0.094	0.307
		GLUC	-0.047	-0.170	0.077	0.461	0.76
RURAL MALES	225/247	PAI-1	0.029	-0.153	0.210	0.756	0.725
		BMI	-0.124	-0.305	0.057	0.178	0.216
		MAP	0.143	-0.038	0.324	0.122	0.677
		TRIG	0.083	-0.098	0.265	0.368	0.204
		GLUC	0.031	-0.150	0.213	0.734	0.428
URBAN FEMALES	957/341	PAI-1	-0.134	-0.258	-0.011	0.033	0.255
		BMI	-0.026	-0.150	0.098	0.68	0.186
		MAP	0.040	-0.103	0.182	0.586	0.011
		TRIG	-0.129	-0.273	0.014	0.077	0.906
		GLUC	-0.126	-0.268	0.017	0.084	0.485
RURAL FEMALES	317/266	PAI-1	0.017	-0.147	0.180	0.841	0.867
		BMI	0.084	-0.079	0.248	0.311	0.057
		MAP	0.006	-0.157	0.170	0.938	0.242
		TRIG	0.182	0.019	0.346	0.029	0.853
		GLUC	0.116	-0.047	0.279	0.164	0.916

Table S2. Pearson partial correlation coefficients between the five components of the metabolic syndrome. (PAI-1 excluded from analysis.)

Trait	Trait	*r*	CI	N	p-value
MAP	**BMI**	0.27	(0.23, 0.31)	2220	<.0001
HDL	**BMI**	-0.11	(-0.15, -0.07)	2220	<.0001
HDL	**MAP**	0.12	(0.07, 0.16)	2220	<.0001
TG	**BMI**	0.16	(0.12, 0.20)	2220	<.0001
TG	**MAP**	0.11	(0.07, 0.15)	2220	<.0001
TG	**HDL**	-0.24	(-0.28, -0.20)	2220	<.0001
GLUC	**BMI**	0.08	(0.04, 0.12)	2220	0.0002
GLUC	**MAP**	0.09	(0.05, 0.13)	2220	<.0001
GLUC	**HDL**	-0.08	(-0.12, -0.04)	2220	<.0001
GLUC	**TRIG**	0.11	(0.07, 0.15)	2220	<.0001

r = Pearson partial correlation coefficient, calculated using residuals after adjustment for age, sex, and residence;

CI = 95% confidence interval;

p-value = probability of *r* if true partial correlation is zero.

Table S3. Pearson partial correlation coefficients between the five components of the metabolic syndrome, by urban or rural residence. (PAI-1 excluded from analysis.)

		Rural				Urban				Homogeneity of Correlation
Trait 1	**Trait 2**	***r***	**CI**	**N**	**p-value**	***r***	**CI**	**N**	**p-value**	**p-value**
MAP	**BMI**	0.24	(0.16, 0.32)	542	<.0001	0.28	(0.24, 0.33)	1678	<.0001	0.3335
HDL	**BMI**	-0.06	(-0.14, 0.02)	542	0.1631	-0.14	(-0.19, -0.09)	1678	<.0001	0.1083
HDL	**MAP**	0.12	(0.04, 0.20)	542	0.0042	0.12	(0.07, 0.17)	1678	<.0001	0.9314
TG	**BMI**	0.09	(0.01, 0.18)	542	0.0297	0.19	(0.14, 0.24)	1678	<.0001	0.0430
TG	**MAP**	0.16	(0.07, 0.24)	542	0.0002	0.09	(0.04, 0.13)	1678	0.0004	0.1449
TG	**HDL**	-0.28	(-0.36, -0.20)	542	<.0001	-0.23	(-0.27, -0.18)	1678	<.0001	0.2250
GLUC	**BMI**	0.13	(0.05, 0.21)	542	0.0021	0.05	(0.01, 0.10)	1678	0.0245	0.1180
GLUC	**MAP**	0.11	(0.02, 0.19)	542	0.0116	0.08	(0.03, 0.13)	1678	0.0011	0.5601
GLUC	**HDL**	-0.09	(-0.17, -0.01)	542	0.0356	-0.08	(-0.13, -0.03)	1678	0.0011	0.8230
GLUC	**TRIG**	0.12	(0.04, 0.20)	542	0.0044	0.11	(0.06, 0.15)	1678	<.0001	0.7341

r = Pearson partial correlation coefficient, calculated using residuals after adjustment for age and sex, by residence;

CI = 95% confidence interval;

p-value = probability that the true partial correlation is zero;

Homogeneity of Correlation p-value = probability of these data if true partial correlation is equal for urban & rural.

Table S4. Pearson partial correlation coefficients between the five components of the metabolic syndrome, by sex. (PAI-1 excluded from analysis.)

		Females				Males				Homogeneity of Correlation
Trait 1	**Trait 2**	***r***	**CI**	**N**	**p-value**	***r***	**CI**	**N**	**p-value**	**p-value**
MAP	**BMI**	0.26	(0.20, 0.31)	1274	<.0001	0.31	(0.25, 0.37)	946	<.0001	0.1710
HDL	**BMI**	-0.12	(-0.17, -0.07)	1274	<.0001	-0.12	(-0.18, -0.05)	946	0.0003	0.9642
HDL	**MAP**	0.13	(0.07, 0.18)	1274	<.0001	0.11	(0.05, 0.18)	946	0.0004	0.7842
TG	**BMI**	0.16	(0.11, 0.21)	1274	<.0001	0.17	(0.11, 0.23)	946	<.0001	0.7575
TG	**MAP**	0.09	(0.03, 0.14)	1274	0.0016	0.12	(0.06, 0.18)	946	0.0002	0.4210
TG	**HDL**	-0.22	(-0.27, -0.17)	1274	<.0001	-0.26	(-0.32, -0.20)	946	<.0001	0.3481
GLUC	**BMI**	0.08	(0.02, 0.13)	1274	0.0060	0.08	(0.02, 0.15)	946	0.0106	0.8846
GLUC	**MAP**	0.08	(0.02, 0.13)	1274	0.0074	0.11	(0.05, 0.17)	946	0.0006	0.4021
GLUC	**HDL**	-0.09	(-0.14, -0.03)	1274	0.0023	-0.08	(-0.14, -0.01)	946	0.0189	0.8331
GLUC	**TRIG**	0.13	(0.08, 0.19)	1274	<.0001	0.08	(0.02, 0.14)	946	0.0141	0.2184

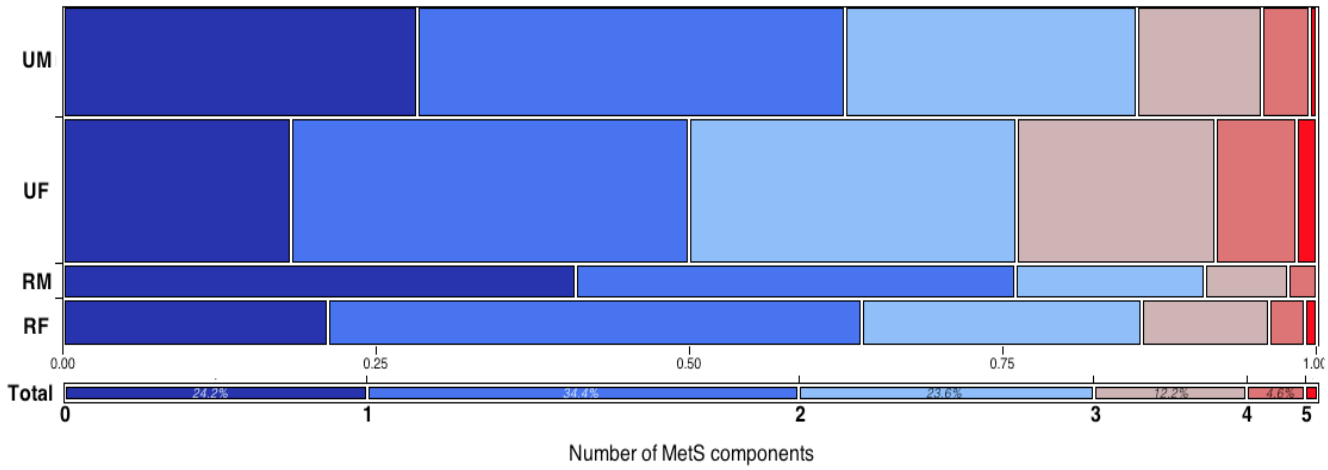
r = Pearson partial correlation coefficient, calculated using residuals after adjustment for age and residence, by sex;

CI = 95% confidence interval;

p-value = probability of *r* if true partial correlation is zero;

Homogeneity of Correlation p-value = probability of these data if true partial correlation is equal for men & women.

Figure S1. Proportions of participants with $N \in [0,5]$ component risk factors of the metabolic syndrome, by sex and environment. Lengths of rectangles represent the percentage of participants with *N* risk factors within each labeled group: Total= all 2220 participants for whom no data were missing; UM = urban males; UF= urban females; RM= rural males; RF= rural females. Areas of rectangles for UM, UF, RM, RF represent proportions with respect to all 2220 participants.



Plasminogen Activator Inhibitor–1 and Diagnosis of the Metabolic Syndrome in a West African Population

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